

6512
1115

#2

OIPE

RAW SEQUENCE LISTING DATE: 11/09/2001
PATENT APPLICATION: US/09/981,124 TIME: 10:23:22

Input Set : A:\es.txt
Output Set: N:\CRF3\11092001\I981124.raw

3 <110> APPLICANT: Green, Allan
4 Singh, Surinder
5 Lenman, Marit
6 Stymne, Sten
8 <120> TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR
IN MODIFYING

9 FATTY ACID METABOLISM
11 <130> FILE REFERENCE: 26-98A
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/981,124 OK
C--> 13 <141> CURRENT FILING DATE: 2001-10-17
13 <150> PRIOR APPLICATION NUMBER: US 09/059769
14 <151> PRIOR FILING DATE: 1998-04-14
16 <150> PRIOR APPLICATION NUMBER: US 60/043706
17 <151> PRIOR FILING DATE: 1997-04-16
19 <150> PRIOR APPLICATION NUMBER: AU P06223
20 <151> PRIOR FILING DATE: 1997-04-15
22 <150> PRIOR APPLICATION NUMBER: AU P06226
23 <151> PRIOR FILING DATE: 1997-04-15
25 <150> PRIOR APPLICATION NUMBER: US 60/050403
26 <151> PRIOR FILING DATE: 1997-06-20
28 <160> NUMBER OF SEQ ID NOS: 24
30 <170> SOFTWARE: PatentIn version 3.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1358
34 <212> TYPE: DNA
35 <213> ORGANISM: Crepis palaestina
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (30)..(1151)
40 <223> OTHER INFORMATION:
43 <400> SEQUENCE: 1

ENTERED

p.5

44 gagaagttga ccataaatca tttatcaac atg ggt gcc ggc ggt cgt ggt cgg 53
45 Met Gly Ala Gly Gly Arg Gly Arg
46 1 5
48 aca tcg gaa aaa tcg gtc atg gaa cgt gtc tca gtt gat cca gta acc 101
49 Thr Ser Glu Lys Ser Val Met Glu Arg Val Ser Val Asp Pro Val Thr
50 10 15 20
52 ttc tca ctg agt gaa ttg aag caa gca atc cct ccc cat tgc ttc cag 149
53 Phe Ser Leu Ser Glu Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln
54 25 30 35 40
56 aga tct gta atc cgc tca tct tac tat gtt gtt caa gat ctc att att 197
57 Arg Ser Val Ile Arg Ser Ser Tyr Tyr Val Val Gln Asp Leu Ile Ile
58 45 50 55
60 gcc tac atc ttc tac ttc ctt gcc aac aca tat atc cct act ctt cct 245
61 Ala Tyr Ile Phe Tyr Phe Leu Ala Asn Thr Tyr Ile Pro Thr Leu Pro
62 60 65 70
64 act agt cta gcc tac tta gct tgg ccc gtt tac tgg ttc tgt caa gct 293
65 Thr Ser Leu Ala Tyr Leu Ala Trp Pro Val Tyr Trp Phe Cys Gln Ala

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66	75	80	85	
68	agc gtc ctc act ggc tta tgg atc ctc ggc cac gaa tgt ggt cac cat			341
69	Ser Val Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His			
70	90	95	100	
72	gcc ttt agc aac tac aca tgg ttt gac gac act gtg ggc ttc atc ctc			389
73	Ala Phe Ser Asn Tyr Thr Trp Phe Asp Asp Thr Val Gly Phe Ile Leu			
74	105	110	115	120
76	cac tca ttt ctc ctc acc ccg tat ttc tct tgg aaa ttc agt cac cgg			437
77	His Ser Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Phe Ser His Arg			
78	125	130	135	
80	aat cac cat tcc aac aca agt tcg att gat aac gat gaa gtt tac att			485
81	Asn His His Ser Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile			
82	140	145	150	
84	ccg aaa agc aag tcc aaa ctc gcg cgt atc tat aaa ctt ctt aac aac			533
85	Pro Lys Ser Lys Ser Lys Leu Ala Arg Ile Tyr Lys Leu Leu Asn Asn			
86	155	160	165	
88	cca cct ggt cgg ctg ttg gtt ttg att atc atg ttc acc cta gga ttt			581
89	Pro Pro Gly Arg Leu Leu Val Leu Ile Ile Met Phe Thr Leu Gly Phe			
90	170	175	180	
92	cct tta tac ctc ttg aca aat att tcc ggc aag aaa tac gac agg ttt			629
93	Pro Leu Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe			
94	185	190	195	200
96	gcc aac cac ttc gac ccc atg agt cca att ttc aaa gaa cgt gag cgg			677
97	Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg			
98	205	210	215	
100	ttt cag gtc ttc ctt tcg gat ctt ggt ctt ctt gcc gtg ttt tat gga			725
101	Phe Gln Val Phe Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly			
102	220	225	230	
104	att aaa gtt gct gta gca aat aaa gga gct gct tgg gta gcg tgc atg			773
105	Ile Lys Val Ala Val Ala Asn Lys Gly Ala Ala Trp Val Ala Cys Met			
106	235	240	245	
108	tat gga gtt ccg gta tta ggc gta ttt acc ttt ttc gat gtg atc acc			821
109	Tyr Gly Val Pro Val Leu Gly Val Phe Thr Phe Phe Asp Val Ile Thr			
110	250	255	260	
112	ttc ttg cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa			869
113	Phe Leu His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu			
114	265	270	275	280
116	tgg aac tgg atc aga ggg gcc ttg tca gca atc gat agg gac ttt gga			917
117	Trp Asn Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Arg Asp Phe Gly			
118	285	290	295	
120	ttc ctg aat agt gtt ttc cat gat gtt aca cac act cat gtc atg cat			965
121	Phe Leu Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His			
122	300	305	310	
124	cat ttg ttt tca tac att cca cac tat cat gca aag gag gca agg gat			1013
125	His Leu Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp			
126	315	320	325	
128	gca atc aag cca atc ttg ggc gac ttt tat atg atc gac agg act cca			1061
129	Ala Ile Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro			
130	330	335	340	

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132 att tta aaa gca atg tgg aga gag ggc agg gag tgc atg tac atc gag      1109
133 ile leu lys ala met trp arg glu gly arg glu cys met tyr ile glu
134 345                      350                      355                      360
136 cct gat agc aag ctc aaa ggt gtt tat tgg tat cat aaa ttg      1151
137 pro asp ser lys leu lys gly val tyr trp tyr his lys leu
138                      365                      370
140 tgatcatatg caaaatgcac atgcattttc aaaccctcta gttacgtttg ttctatgtat      1211
142 aataaaccgc cggctctttg gttgactatg cctaagccag gcgaaacagt taaataatat      1271
144 cggtatgatg tgtaatgaaa gtatgtggtt gtctggtttt gttgctatga aagaaagtat      1331
146 gtggttgtcg gtcaaaaaaa aaaaaaa      1358
149 <210> SEQ ID NO: 2
150 <211> LENGTH: 374
151 <212> TYPE: PRT
152 <213> ORGANISM: Crepis palaestina
154 <400> SEQUENCE: 2
156 Met Gly Ala Gly Gly Arg Gly Arg Thr Ser Glu Lys Ser Val Met Glu
157 1                      5                      10                      15
160 Arg Val Ser Val Asp Pro Val Thr Phe Ser Leu Ser Glu Leu Lys Gln
161                      20                      25                      30
164 Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr
165                      35                      40                      45
168 Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala
169                      50                      55                      60
172 Asn Thr Tyr Ile Pro Thr Leu Pro Thr Ser Leu Ala Tyr Leu Ala Trp
173 65                      70                      75                      80
176 Pro Val Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile
177                      85                      90                      95
180 Leu Gly His Glu Cys Gly His His Ala Phe Ser Asn Tyr Thr Trp Phe
181                      100                     105                     110
184 Asp Asp Thr Val Gly Phe Ile Leu His Ser Phe Leu Leu Thr Pro Tyr
185                      115                     120                     125
188 Phe Ser Trp Lys Phe Ser His Arg Asn His His Ser Asn Thr Ser Ser
189                      130                     135                     140
192 Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala
193 145                      150                     155                     160
196 Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu
197                      165                     170                     175
200 Ile Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile
201                      180                     185                     190
204 Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser
205                      195                     200                     205
208 Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu
209                      210                     215                     220
212 Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys
213 225                      230                     235                     240
216 Gly Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val
217                      245                     250                     255
220 Phe Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser
221                      260                     265                     270

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TIME: 10:23:22

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Output Set: N:\CRF3\11092001\I981124.raw

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224 Ser Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu
225           275           280           285
228 Ser Ala Ile Asp Arg Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp
229   290           295           300
232 Val Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His
233 305           310           315           320
236 Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp
237           325           330           335
240 Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu
241           340           345           350
244 Gly Arg Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Leu Lys Gly Val
245   355           360           365
248 Tyr Trp Tyr His Lys Leu
249   370
252 <210> SEQ ID NO: 3
253 <211> LENGTH: 1309
254 <212> TYPE: DNA
255 <213> ORGANISM: Crepis sp.
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (937)..(937)
260 <223> OTHER INFORMATION: N is any nucleotide residue
263 <220> FEATURE:
264 <221> NAME/KEY: CDS
265 <222> LOCATION: (26)..(1147)
266 <223> OTHER INFORMATION:
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (901)..(901)
272 <223> OTHER INFORMATION: N is any nucleotide residue
275 <400> SEQUENCE: 3
276 tggtgacat aatcatcta tcaac atg ggt gcc ggc ggc cgt ggt cgg tcg           52
277                               Met Gly Ala Gly Gly Arg Gly Arg Ser
278                               1                               5
280 gaa aag tcg gtc atg gaa cgt gtc tca gtt gat cca gta acc ttc tca           100
281 Glu Lys Ser Val Met Glu Arg Val Ser Val Asp Pro Val Thr Phe Ser
282 10                               15                               20                               25
284 ctg agt gat ttg aag caa gca atc cct cca cat tgc ttc cag cga tct           148
285 Leu Ser Asp Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln Arg Ser
286                               30                               35                               40
288 gtc atc cgt tca tct tat tac gtt gtt cag gat ctc ata att gcc tac           196
289 Val Ile Arg Ser Ser Tyr Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr
290                               45                               50                               55
292 atc ttc tac ttc ctt gcc aac aca tat atc cct aat ctc cct cat cct           244
293 Ile Phe Tyr Phe Leu Ala Asn Thr Tyr Ile Pro Asn Leu Pro His Pro
294   60                               65                               70
296 cta gcc tac tta gct tgg ccg ctt tac tgg ttc tgt caa gct agc gtc           292
297 Leu Ala Tyr Leu Ala Trp Pro Leu Tyr Trp Phe Cys Gln Ala Ser Val
298   75                               80                               85

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Input Set : A:\es.txt

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```

300 ctc act ggg tta tgg atc ctc ggc cat gaa tgt ggt cac cat gcc tat      340
301 Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His Ala Tyr
302 90                               95                               100                               105
304 agc aac tac aca tgg gtt gac gac act gtg ggc ttc atc atc cat tca      388
305 Ser Asn Tyr Thr Trp Val Asp Asp Thr Val Gly Phe Ile Ile His Ser
306                               110                               115                               120
308 ttt ctc ctc acc ccg tat ttc tct tgg aaa tac agt cac cgg aat cac      436
309 Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His
310                               125                               130                               135
312 cat tcc aac aca agt tcg att gat aac gat gaa gtt tac att ccg aaa      484
313 His Ser Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys
314                               140                               145                               150
316 agc aag tcc aaa ctc aag cgt atc tat aaa ctt ctt aac aac cca cct      532
317 Ser Lys Ser Lys Leu Lys Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro
318                               155                               160                               165
320 ggt cga ctg ttg gtt ttg gtt atc atg ttc acc cta gga ttt cct tta      580
321 Gly Arg Leu Leu Val Leu Val Ile Met Phe Thr Leu Gly Phe Pro Leu
322 170                               175                               180                               185
324 tac ctc ttg aca aat att tcc ggc aag aaa tac gat agg ttt gcc aac      628
325 Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn
326                               190                               195                               200
328 cac ttc gac ccc atg agt cca att ttc aaa gaa cgt gag cgg ttt cag      676
329 His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln
330                               205                               210                               215
332 gtc ttc ctt tcg gat ctt ggt ctt ctt gct gtg ttt tat gga att aaa      724
333 Val Phe Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys
334                               220                               225                               230
336 gtt gct gta gca aat aaa gga gct gct tgg gtg gcg tgc atg tat gga      772
337 Val Ala Val Ala Asn Lys Gly Ala Ala Trp Val Ala Cys Met Tyr Gly
338                               235                               240                               245
340 gtt ccg gtg cta ggc gta ttt acc ttt ttc gat gtg atc acg ttc tta      820
341 Val Pro Val Leu Gly Val Phe Thr Phe Phe Asp Val Ile Thr Phe Leu
342 250                               255                               260                               265
344 cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa tgg aac      868
345 His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu Trp Asn
346                               270                               275                               280
W--> 348 tgg atc aga ggg gct ttg tca gca atc gat agn gac ttt ggg ttc ctg      916
W--> 349 Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Xaa Asp Phe Gly Phe Leu
350                               285                               290                               295
W--> 352 aat agt gtt ttc cat gat gtn aca cac act cac gtc atg cat cat ttg      964
353 Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His His Leu
354                               300                               305                               310
356 ttt tca tac att cca cac tat cat gca aag gaa gca agg gat gca atc      1012
357 Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile
358                               315                               320                               325
360 aaa ccg atc ttg ggc gac ttt tat atg atc gat agg act cca att tta      1060
361 Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu
362 330                               335                               340                               345
364 aaa gca atg tgg aga gag ggc agg gaa tgc atg tac atc gag cct gat      1108

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,124

DATE: 11/09/2001

TIME: 10:23:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11092001\I981124.raw

- L:13 M:270 C: Current Application Number differs, Replaced Current Application No
- L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
- L:348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
- L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
- L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
- L:473 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
- L:1561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
- L:1580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
- L:1598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
- L:1616 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24